WHAT IS CLAIMED IS:

1. A method for improving the reliability of physical measurements obtained from array hybridization studies performed on an array having a large number of genomic samples, each composed of a small number of replicates insufficient for making precise and valid statistical inferences, comprising the step of estimating an error in measurement of a sample by averaging errors obtained when measuring the large number of samples, and utilizing the estimated sample error as a standard for accepting or rejecting the measurement of the respective sample.

2. The method of claim 1 wherein a physical measurement quantity determined from an entire array population is used to estimate discrete instances of that quantity for the small number of replicate samples within that population.

3. The method of claim 1 wherein the estimates of measurement error are used to plan, manage and control array hybridization studies on the basis of (a) the probability of detecting a true difference of specified magnitude between physical measurements of a given number of replicates, or (b) the number of replicates required to detect a true difference of specified magnitude.

4. A method in which outlier measurements are identified using measurement error estimates arrived at as in claim 1.

5. A method for discriminating among response classes of physical measurements obtained in hybridization studies, such as signal and non-signal, within hybridization arrays, comprising the steps deriving distributions of data obtained from the

physical measurements and deconvolving overlapping portions of distributions.

6. The method of claim 5 wherein one of dual and multiple distributions derived from a measured array are modeled by mixture modeling.

7. The method of claim 5 wherein mixture modeling is used to determine the probability that any discrete array element falls within one of the modeled distributions.

8. The method of claim 1, used to evaluate physical measurements obtained from biological and chemical assays conducted on one of substrates, substrates containing wells, and test tubes.

9. The method of claim 3 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.

10. The method of claim 4 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.

11. The method of claim 7 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.

12. The method of claim 2 wherein the estimates of measurement error are used to plan, manage and control array

hybridization studies on the basis of (a) the probability of detecting a true difference of specified magnitude between physical measurements of a given number of replicates, or (b) the number of replicates required to detect a true difference of specified magnitude.

13. A method in which outlier measurements are identified using measurement error estimates arrived at as in claim 2.

14. The method of claim 6 wherein mixture modeling is used to determine the probability that any discrete array element falls within one of the modeled distributions.

15. The method of claim 2, used to evaluate physical measurements obtained from biological and chemical assays conducted on one of substrates, substrates containing wells, and test tubes.

16. The method of claim 5, used to evaluate physical measurements obtained from biological and chemical assays conducted on one of substrates, substrates containing wells, and test tubes.

17. The method of claim 6, used to evaluate physical measurements obtained from biological and chemical assays conducted on one of substrates, substrates containing wells, and test tubes.